

IN THE SPECIFICATION:

A. Please replace the paragraph beginning on page 20, line 19, with the following paragraph, with added matters shown by underlining:

The 5' untranslated region contains a promoter or RNA polymerase binding sequence, such as those for the T7, T3, or SP6 RNA polymerase. Positioned downstream of or within the promoter region is a DNA sequence, which codes for a ribosomal binding site. This ribosome binding site may be specific for prokaryotic ribosomal complexes (including ribosomal RNAs) if a prokaryotic translation procedure is used. However, a preferred embodiment of this invention uses a eukaryotic sequence and an in vitro eukaryotic translation system, such as the rabbit reticulocyte system (Krawetz *et al.*, 1983 *Can. J. Biochem. Cell. Biol.* 61:274-286; Merrick, 1983 *Meth. Enzymol.* 101:38). A consensus translation initiation sequence, GCCGCCACCATGG, (SEQ ID NO: 33), as well as other functionally related sequences have been established for vertebrate mRNAs (Kozak, 1987 *Nucleic Acids Res.* 15:8125-8148). This sequence or related sequences may be used in the DNA construction to direct protein synthesis in vitro. The ATG triplet in this initiation sequence is the translation initiation codon for methionine; in vitro protein synthesis is expected to begin at this point.

B. Please replace the paragraph beginning on page 77, line 20, with the following paragraph, with added matters shown by underlining:

The binding of mutated phage clones to immobilized Flt-1 receptor was analyzed by ELISA as described in Example 17.

Table 14.

Clone	Insert sequence	SEQ ID NO.	Binding to hFlt-1 in %
V5.2	NGYEIEWYSWVTHGMY (Asn-Gly-Tyr-Glu-Ile-Glu-Trp-Tyr-Ser-Trp-Val-Thr-His-Gly-Met-Tyr)	1	100
N1/A	AGYEIEWYSWVTHGMY (Ala-Gly-Tyr-Glu-Ile-Glu-Trp-Tyr-Ser-Trp-Val-Thr-His-Gly-Met-Tyr)	14	42.93 ± 25.76
E4/A	NGYAIIEWYSWVTHGMY (Asn-Gly-Tyr-Ala-Ile-Glu-Trp-Tyr-Ser-Trp-Val-Thr-His-Gly-Met-Tyr)	15	17.54 ± 5.31
I5/A	NGYEAEWYSWVTHGMY (Asn-Gly-Tyr-Glu-Ile-Glu-Ala-Tyr-Ser-Trp-Val-Thr-His-Gly-Met-Tyr)	16	18.76 ± 0.26
E6/A	NGYEIAWYSWVTHGMY (Asn-Gly-Tyr-Glu-Ile-Ala-Trp-Tyr-Ser-Trp-Val-Thr-His-Gly-Met-Tyr)	17	19.155 ± 14.07
W7/A	NGYEIEAYSWVTHGMY (Asn-Gly-Tyr-Glu-Ile-Glu-Ala-Tyr-Ser-Trp-Val-Thr-His-Gly-Met-Tyr)	18	66.23 ± 27.07
Y8/A	NGYEIEWASWVTHGMY (Asn - Gly - Tyr - Glu - Ile - Glu - Trp - Ala - Ser - Trp - Val - Thr - His - Gly - Met - Tyr)	19	67.035 ± 6.28
S9/A	NGYEIEWYAWVTHGMY (Asn - Gly - Tyr - Glu - Ile - Glu - Trp - Tyr - Ala - Trp - Val - Thr - His - Gly - Met - Tyr)	20	101.69 ± 16.70
W10/A	NGYEIEWYSAVTHGMY (Asn - Gly - Tyr - Glu - Ile - Glu - Trp - Tyr - Ala - Trp - Val - Thr - His - Gly - Met - Tyr)	21	22.08 ± 7.19
T12/A	NGYEIEWYSWVAHGMY (Asn - Gly - Tyr - Glu - Ile - Glu - Trp - Tyr - Ser - Trp - Val - Ala - His - Gly - Met - Tyr)	22	62.63 ± 22.58
H13/A	NGYEIEWYSWVTAGMY (Asn - Gly - Tyr - Glu - Ile - Glu - Trp - Tyr - Ser - Trp - Val - Thr - Ala - Gly - Met - Tyr)	23	55.34 ± 10.78
M15/A	NGYEIEWYSWVTHGAY (Asn - Gly - Tyr - Glu - Ile - Glu - Trp - Tyr - Ser - Trp - Val - Thr - His - Gly - Ala - Tyr)	24	78.24 ± 19.42
Y16/A	NGYEIEWYSWVTHGMA (Asn - Gly - Tyr - Glu - Ile - Glu - Trp - Tyr - Ser - Trp - Val - Thr - His - Gly - Met - Ala)	25	15.30 ± 15.27

E46/ A	NGYAIAWYSWVTHGMY (Asn - Gly - Tyr - Ala - Ile - Ala - Trp - Tyr - Ser - Trp - Val - Thr - His - Gly - Met - Tyr)	<u>26</u>	44.46 ± 7.05
W710 /A	NGYEIEAYSAVTGMY (Asn - Gly - Tyr - Glu - Ile - Glu - Ala - Tyr - Ser - Ala - Val - Thr - His - Gly - Met - Tyr)	<u>27</u>	62.15 ± 22.16
V5.2/ 1	EIEWYSW (Glu - Ile - Glu - Trp - Tyr - Ser - Trp)	<u>28</u>	6.55 ±15.81
V5.2/ 5	EIEWYSWVTHGMY (Glu - Ile - Glu - Trp - Tyr - Ser - Trp - Val - Thr - His - Gly - Met - Tyr)	<u>29</u>	85.6 ± 22.61

**C. Please enter the paper copy of the Sequence Listing submitted herein into the specification,
in replacement of the Sequence Listing submitted previously.**

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